Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application:

1-4. (canceled)

5. (currently amended) A method for detecting a first nucleotide sequence which differs from a second nucleotide sequence comprising:

providing a sample potentially containing the first and second nucleotide sequences;

providing a first oligonucleotide set of at least two oligonucleotides suitable for ligation together at a first ligation junction and for hybridization without mismatch to the first nucleotide sequence but not to the second nucleotide sequence, wherein the at least two oligonucleotides hybridize on the first nucleotide sequence and the distinguishing nucleotide is complementary to the oligonucleotide of the first oligonucleotide set having its 3' end at the first ligation junction;

providing a thermocyclable ligase which does not become irreversibly denatured and lose its catalytic activity when subjected to temperatures ranging from about 50° C. to 105° C.;

blending the sample, the first oligonucleotide set, and the ligase to form an amplification mixture;

subjecting the amplification mixture to a series of cycles comprising a denaturation treatment, and a thermal hybridization treatment; and

detecting the presence of the first nucleotide sequence in the sample by detecting the presence of ligated oligonucleotides of the first oligonucleotide set.

6-8. (canceled)

9. (new) The method according to claim 5, wherein said subjecting amplifies the sequence of nucleotides complementary to the first nucleotide sequence by about 50 to about 500 fold more than if a single base mismatch were present at the first ligation junction.

10. (new) The method according to claim 5, wherein said subjecting amplifies the sequence of nucleotides complementary to the first nucleotide sequence by at least about 100 fold more than if the first nucleotide sequence were not present in the sample.

11. (new) The method according to claim 5, wherein said subjecting is repeated for 5 to 20 cycles.

12. (new) The method according to claim 5, wherein the first nucleotide sequence can be distinguished in the sample when present in an amount down to 1 femtomole.

13. (new) The method according to claim 5, wherein the thermal hybridization step discriminates between the first nucleotide sequence and the second nucleotide sequence based on a distinguishing nucleotide at the first ligation junction.

14. (new) The method according to claim 13, wherein the difference between the first and second nucleotide sequences is a single nucleic acid base pair change.

15. (new) The method according to claim 13, wherein the difference between the first and second nucleotide sequences is a nucleic acid deletion.

16. (new) The method according to claim 13, wherein the difference between the first and second nucleotide sequences is a nucleic acid insertion.

17. (new) The method according to claim 13, wherein A:A mismatches at the distinguishing nucleotide have a mismatched/complementary percentage of 0.4 to <0.1%.

18. (new) The method according to claim 13, wherein T:T mismatches at the distinguishing nucleotide have a mismatched/complementary percentage of 0.7 to 1.0%.

19. (new) The method according to claim 13, wherein G:T mismatches at the distinguishing nucleotide have a mismatched/complementary percentage of 1.0 to 1.5%.

20. (new) The method according to claim 13, wherein C:T mismatches at the distinguishing nucleotide have a mismatched/complementary percentage of 0.4 to <0.1%.

21. (new) The method according to claim 13, wherein G:A mismatches at the distinguishing nucleotide have a mismatched/complementary percentage of 0.4 to <0.1%.

22. (new) The method according to claim 13, wherein C:A mismatches at the distinguishing nucleotide have a mismatched/complementary percentage of 0.4 to <0.1%.

23. (new) The method according to claim 5, further comprising:

amplifying the first nucleotide sequence in the sample prior to said blending by subjecting the sample to a polymerase chain reaction process.

24. (new) The method according to claim 5, wherein said detecting comprises:

capturing a hook attached to at least one of the oligonucleotides of the first oligonucleotide set.

25. (new) The method according to claim 5, wherein said detecting comprises:

detecting a label attached to at least one of the oligonucleotides of the first oligonucleotide set.

26. (new) The method according to claim 5, wherein said detecting comprises:

separating products of said subjecting by size.

27. (new) The method according to claim 5, wherein the oligonucleotides of the first oligonucleotide set each have a hybridization temperature of about 66° C. to 70° C.